



## SEQUENCE LISTING

<110> DERBRAH, KNUTZON  
WIKERJI, PRADIP  
HUANG, YUNG-SHENG  
THURMOND, JENNIFER  
CHAUDHARY, SUNITA  
LEONARD, AMANDA

<120> Methods and Compositions for Synthesis of Long Chain  
Polyunsaturated Fatty Acids

<130> CGAB-210 USA

<140> US 09/367,013

<141> 1999-08-05

<150> US 08/834,655

<151> 1997-04-11

<160> 40

<170> PatentIn version 3.0

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<212> DNA

<213> Mortierella alpina

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<221> misc\_feature

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<223> Description of Combined DNA/RNA Molecule: Delta-6 Desaturase  
Nucleic Acid Sequence

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 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu  
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385					390					395					400
Phe	Pro	Ser	Met	Pro	Arg	His	Asn	Phe	Ser	Lys	Ile	Gln	Pro	Ala	Val
				405					410					415	
Glu	Thr	Leu	Cys	Lys	Lys	Tyr	Asn	Val	Arg	Tyr	His	Thr	Thr	Gly	Met
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Ile	Glu	Gly	Thr	Ala	Glu	Val	Phe	Ser	Arg	Leu	Asn	Glu	Val	Ser	Lys
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Glu	Asn	Ala	Ala	Ala	Ala	Val	Gln	Glu	Glu	Asp	Met	Ser	Val	His	Leu	
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Val	Thr	Lys	Tyr	Tyr	Ile	Val	Pro	Tyr	Leu	Phe	Val	Asn	Phe	Trp	Leu	
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Thr His Val Ala His	His Leu Phe Ser Gln	Met Pro Phe Tyr His Ala		
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Glu Glu Ala Thr Tyr	His Leu Lys Lys Leu	Gly Glu Tyr Tyr Val		
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Tyr Asp Pro Ser Pro	Ile Val Val Ala Val	Trp Arg Ser Phe Arg Glu		
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Cys Gly Trp Leu Ala	His Asp Phe Leu His	His Gln Val Phe Gln Asp		
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Arg Phe Trp Gly Asp	Leu Phe Gly Ala Phe	Leu Gly Gly Val Cys Gln		
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Gly Phe Ser Ser Ser	Trp Trp Lys Asp Lys	His Asn Thr His His Ala		
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Glu Glu Leu Thr Arg	Met Trp Ser Arg Phe	Met Val Leu Asn Gln Thr		
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Trp Phe Tyr Phe Pro	Ile Leu Ser Phe Ala	Arg Leu Ser Trp Cys Leu		
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Gln Ser Ile Leu Phe	Val Leu Pro Asn Gly	Gln Ala His Lys Pro Ser		

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Val	Phe	Ser	Arg	Leu	Asn	Glu	Val	Ser	Lys	Ala	Ala	Ser	Lys	Met	Gly
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 <223> Amino acids 27, 48, and 63 uncertain of sequence

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Ala	Gly	Leu	Leu	Gly	Leu	Leu	Trp	Ile	Gln	Ser	Ala	Tyr	Ile	Gly	Xaa
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Asp	Ser	Gly	His	Tyr	Val	Ile	Met	Ser	Asn	Lys	Ser	Asn	Asn	Xaa	Phe
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Ala	Gln	Leu	Leu	Ser	Gly	Asn	Cys	Leu	Thr	Gly	Ile	Ile	Ala	Trp	Trp

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Gly	His	Asp	Ser	Gly	His	Tyr	Val	Ile	Met	Ser	Asn	Lys	Ser	Tyr	Asn
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Ala	Trp	Trp	Lys	Trp	Thr	His	Asn	Ala	His	His	Leu	Ala	Cys	Asn	Ser
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Leu	Asp	Tyr	Asp	Pro	Asp	Leu	Gln	His	Ile	Pro	Val	Phe	Ala	Val	Ser
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Thr	Lys	Phe	Phe	Ser	Ser	Leu	Thr	Ser	Arg	Phe	Tyr	Asp	Arg	Lys	Leu
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145					150					155					160
Phe	Ala	Gly	Ile	Leu	Val	Phe	Trp	Thr	Trp	Phe	Pro	Leu	Leu	Val	Ser
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Cys	Leu	Pro	Asn	Trp	Pro	Glu	Arg	Phe	Phe	Phe	Val	Phe	Thr	Ser	Phe
			180					185					190		
Thr	Val	Thr	Ala	Leu	Gln	His	Ile	Gln	Phe	Thr	Leu	Asn	His	Phe	Ala
		195					200					205			
Ala	Asp	Val	Tyr	Val	Gly	Pro	Pro	Thr	Gly	Ser	Asp	Trp	Phe	Glu	Lys
	210					215					220				
Gln	Ala	Ala	Gly	Thr	Ile	Asp	Ile	Ser	Cys	Arg	Ser	Tyr	Met	Asp	Trp
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 <223> Amino acids 2, 3, 30, 121, and 125 uncertain of sequence.

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Phe	Thr	Gly	Phe	Thr	Val	Thr	Ala	Leu	Gln	His	Ile	Gln	Phe	Thr	Leu
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Asn	His	Phe	Ala	Ala	Asp	Val	Tyr	Val	Gly	Pro	Pro	Thr	Gly	Ser	Asp
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Trp	Phe	Glu	Lys	Gln	Ala	Ala	Gly	Thr	Ile	Asp	Ile	Ser	Cys	Arg	Ser
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Tyr	Met	Asp	Trp	Phe	Phe	Cys	Gly	Leu	Gln	Phe	Gln	Leu	Glu	His	His
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Leu	Phe	Pro	Arg	Leu	Pro	Arg	Cys	His	Leu	Arg	Lys	Val	Ser	Pro	Val
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Gly	Gln	Arg	Gly	Phe	Gln	Arg	Lys	Xaa	Asn	Leu	Ser	Xaa			
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 <223> Amino acid at 110 uncertain of sequence

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			20					25					30		
Gly	Leu	Phe	Phe	Ile	Val	Arg	Phe	Leu	Glu	Ser	Asn	Trp	Phe	Val	Trp
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Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn  
50 55 60

Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys  
65 70 75 80

Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu  
85 90 95

His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala  
100 105 110

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Lys Pro Leu  
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Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val  
35 40 45

Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr  
50 55 60

Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu  
65 70 75 80

Leu Val Gln Ala Lys Ala Ala  
85

<210> 11

<211> 143

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(143)

<223> Amino acid 125 uncertain of sequence

<400> 11

Arg His Glu Ala Ala Arg Gly Gly Thr Arg Leu Ala Tyr Met Leu Val  
1 5 10 15

Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg  
20 25 30

Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu  
           35                          40                          45  
 Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile  
       50                          55                          60  
 Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg  
   65                          70                          75                          80  
 Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser  
                           85                          90                          95  
 Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His  
                           100                          105                          110  
 His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro  
           115                          120                          125  
 Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val  
       130                          135                          140

<210> 12  
 <211> 35  
 <212> DNA  
 <213> Artificial/Unknown  
  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Description of Artificial Sequence: PCR Primer

<400> 12  
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35

<210> 13  
 <211> 33  
 <212> DNA  
 <213> Artificial/Unknown  
  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Description of Combined RNA/DNA Molecule:PCR Primer

<400> 13  
 cuacuacuac uaggagtcct ctacggtggt ttg

33

<210> 14  
 <211> 33  
 <212> DNA  
 <213> Artificial/Unknown  
  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Description of Combined RNA/DNA Molecule:PCR Primer

<400> 14  
caucaucauc auatgatgct caagctgaaa ctg 33

<210> 15  
<211> 39  
<212> DNA  
<213> Artificial/Unknown

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence: PCR Primer

<400> 15  
taccaactcg agaaaatggc tgctgctccc agtgtgagg 39

<210> 16  
<211> 39  
<212> DNA  
<213> Artificial/Unknown

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence:PCR Primer

<400> 16  
aactgatcta gattactgcg ccttacccat cttggaggc 39

<210> 17  
<211> 39  
<212> DNA  
<213> Artificial/Unknown

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence:PCR Primer

<400> 17  
taccaactcg agaaaatggc acctcccaac actatcgat 39

<210> 18  
<211> 39  
<212> DNA  
<213> Artificial/Unknown

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence:PCR Primer

<400> 18  
aactgatcta gattacttct tgaaaaagac cacgtctcc 39

<210> 19  
<211> 746  
<212> DNA  
<213> Dictyostelium discoideum

<400> 19  
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cactcctcta tggattttac aactcctaat atcgactca agattgggaa gcttttgtaa 120  
aggatggtaa aaatgggtgca attcgtgtta gtgtcgccac aaatttcgat aaggccgctt 180  
acgtcattgg taaattgtct tttgttttct tccgtttcat ccttccactc cgttatcata 240  
gctttacaga tttaatttgt tatttccctca ttgctgaatt cgtcttttgg tggatatctca 300  
caattaattt ccaagttagt catgtcgctg aagatctcaa attctttgct acccctgaaa 360  
gaccagatga accatctcaa atcaatgaag attgggcaat ccttcaactt aaaactactc 420  
aagattatgg tcatgggtca ctcttttgta ctttttttag tggttcttta aatcatcaag 480  
ttgttcatca tttattccca tcaattgtc aagatttcta ccacaaactt gtaccaattg 540  
taaaagaagt ttgtaaagaa cataacatta cttaccacat taaaccaaac ttcactgaag 600  
ctattatgtc acacattaat tacctttaca aaatgggttaa tgatccagat tatgttaaaa 660  
aaccattagc ctcaaaagat gattaaatga aataacttaa aaaccaatta tttacttttg 720  
acaaacagta atattaataa atacaa 746

<210> 20  
<211> 228  
<212> PRT  
<213> Dictyostelium discoideum

<220>  
<221> UNSURE  
<222> (1)..(228)  
<223> Amino acid 228 uncertain of sequence

<400> 20

Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln His  
1 5 10 15

Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr Arg Thr  
20 25 30

Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly Ala Ile Arg  
35 40 45

Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr Val Ile Gly Lys

50	55	60
Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro Leu Arg Tyr His Ser		
65	70	75 80
Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile Ala Glu Phe Val Phe Gly		
	85	90 95
Trp Tyr Leu Thr Ile Asn Phe Gln Val Ser His Val Ala Glu Asp Leu		
	100	105 110
Lys Phe Phe Ala Thr Pro Glu Arg Pro Asp Glu Pro Ser Gln Ile Asn		
	115	120 125
Glu Asp Trp Ala Ile Leu Gln Leu Lys Thr Thr Gln Asp Tyr Gly His		
	130	135 140
Gly Ser Leu Leu Cys Thr Phe Phe Ser Gly Ser Leu Asn His Gln Val		
145	150	155 160
Val His His Leu Phe Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu		
	165	170 175
Val Pro Ile Val Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His		
	180	185 190
Ile Lys Pro Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu		
	195	200 205
Tyr Lys Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser		
	210	215 220
Lys Asp Asp Xaa		
225		

<210> 21  
 <211> 494  
 <212> DNA  
 <213> *Phaeodactylum tricornutum*  
  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> n at positions 11,20,29,31,40,53,453,489 may be a, c, g, or t

<400> 21	
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cccccaagc cttttgtcga ctggttctgt ggtggcttcc agtaccaagt cgaccaccac	120
ttattcccca gcctgccccg acacaatctg gccaaagacac acgcactggg cgaatcgttc	180
tgcaaggagt ggggtgtcca gtaccacgaa gccgacctcg tggacgggac catggaagtc	240
ttgcaccatt tgggcagcgt ggccggcgaa ttcgtcgtgg attttgtacg cgacggaccc	300
gccatgtaat cgtcgttctgt gacgatgcaa gggttcacgc acatctacac aactcactc	360
acacaactag tgtaactcgt atagaattcg gtgtcgacct ggaccttggt tgactgggtg	420

gggatagggt aggtaggcgg acgcgtgggt cgnccccggg aattctgtga ccggtacctg 480  
gccccgcgtna aagt 494

<210> 22  
<211> 102  
<212> PRT  
<213> Phaeodactylum tricornutum

<220>  
<221> UNSURE  
<222> (1)..(102)  
<223> Amino acids 4,7,10,11,14, and 18 uncertain of sequence

<400> 22

Phe	Trp	Lys	Xaa	Pro	Ser	Xaa	Pro	Arg	Xaa	Xaa	Gln	Val	Xaa	Gly	Ala
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Glu	Xaa	Gly	Phe	Pro	Pro	Lys	Pro	Phe	Val	Asp	Trp	Phe	Cys	Gly	Gly
			20					25					30		
Phe	Gln	Tyr	Gln	Val	Asp	His	His	Leu	Phe	Pro	Ser	Leu	Pro	Arg	His
			35				40					45			
Asn	Leu	Ala	Lys	Thr	His	Ala	Leu	Val	Glu	Ser	Phe	Cys	Lys	Glu	Trp
	50					55					60				
Gly	Val	Gln	Tyr	His	Glu	Ala	Asp	Leu	Val	Asp	Gly	Thr	Met	Glu	Val
65					70					75				80	
Leu	His	His	Leu	Gly	Ser	Val	Ala	Gly	Glu	Phe	Val	Val	Asp	Phe	Val
			85						90					95	
Arg	Asp	Gly	Pro	Ala	Met										
			100												

<210> 23  
<211> 520  
<212> DNA  
<213> Artificial/Unknown

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 23	
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cttgggtaca cgccggggca gtcgttgggc atgtacttgt gcgcctttgg tctcggtgc	120
atttacattt ttctgcagtt cgccgtaagt cacaccatt tgcccgtag caaccggag	180
gatcagctgc attggctcga gtacgcgcgg accacactgt gaacatcagc accaagtcgt	240
ggtttgtcac atggtggatg tcgaacctca actttcagat cgagcaccac cttttcccca	300

cggcgccccca gttccgtttc aaggagatca gcccgcgcggt cgaggccctc ttcaagcgcc 360  
acgggtctccc ttactacgac atgccctaca cgagcgccgt ctccaccacc ttgccaacc 420  
tctactccgt cgccattcc gtcggcgacg ccaagcgga ctagcctctt ttcctagacc 480  
ttaattcccc accccacccc atgttctgtc ttcctccgc 520

<210> 24  
<211> 153  
<212> PRT  
<213> Artificial/Unknown  
<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 24

Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys Arg  
1 5 10 15  
His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His Val Leu  
20 25 30  
Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala Val Arg Arg  
35 40 45  
Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly Ser Ala Ala Leu  
50 55 60  
Ala Arg Val Arg Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp  
65 70 75 80  
Phe Val Thr Trp Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His  
85 90 95  
Leu Phe Pro Thr Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg  
100 105 110  
Val Glu Ala Leu Phe Lys Arg His Gly Leu Pro Tyr Tyr Asp Met Pro  
115 120 125  
Tyr Thr Ser Ala Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly  
130 135 140  
His Ser Val Gly Asp Ala Lys Arg Asp  
145 150

<210> 25  
<211> 420  
<212> DNA  
<213> Artificial/Unknown  
<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone



<400> 25  
acgcgtccgc ccacgcgtcc gccgcgagca actcatcaag gaaggctact ttgaccctc . 60  
gctcccgcac atgacgtacc gcgtggtcga gattgttggt ctcttcgtgc tttccttttg 120  
gctgatgggt cagtcttcac cctcgcgct cgctctcggc attgtcgtca gcggcatctc 180  
tcagggtcgc tgcggctggg taatgcatga gatgggccat gggtcgttca ctgggtgcat 240  
ttggcttgac gaccggttgt gcgagttctt ttacggcggt ggttgtggca tgagcgggtca 300  
ttactggaaa aaccagcaca gcaaacacca cgcagcgcca aaccggctcg agcacgatgt 360  
agatctcaac accttgccat tgggtggcctt caacgagcgc gtcgtgcgca aggtccgacc 420

<210> 26  
<211> 140  
<212> PRT  
<213> Artificial/Unknown  
<220>  
<221> misc\_feature  
<222> ()..()  
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 26  
Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly Tyr  
1 5 10 15  
Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu Ile Val  
20 25 30  
Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser Ser Pro Leu  
35 40 45  
Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser Gln Gly Arg Cys  
50 55 60  
Gly Trp Val Met His Glu Met Gly His Gly Ser Phe Thr Gly Val Ile  
65 70 75 80  
Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe Tyr Gly Val Gly Cys Gly  
85 90 95  
Met Ser Gly His Tyr Trp Lys Asn Gln His Ser Lys His His Ala Ala  
100 105 110  
Pro Asn Arg Leu Glu His Asp Val Asp Leu Asn Thr Leu Pro Leu Val  
115 120 125  
Ala Phe Asn Glu Arg Val Val Arg Lys Val Arg Pro  
130 135 140

<210> 27  
<211> 1219  
<212> DNA

<213> Homo sapiens

<400> 27

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ttacatagta aaagacttgg actggaaatg ggtcatattt ggggcctatg cgtttggcag      180
ttgcattaac cactcaatga ctctggctat tcatgagatt gccacaatg ctgccttttg      240
caactgcaaa gcaatgtgga atcgctgggt tggaatgttt gctaattctt ctattgggat      300
tccatattca atttccttta agaggtatca catggatcat catcggtacc ttggagctga      360
tggcgctcgat gtagatattc ctaccgattt tgagggctgg ttcttctgta ccgctttcag      420
aaagtttata tgggttattc ttcagcctct cttttatgcc ttctgacctc tgttcatcaa      480
cccaaacca attacgtatc tggaagttat caataccgtg gcacagggtca cttttgacat      540
tttaatttat tacttttttg gaattaaatc cttagtctac atgttggcag catctttact      600
tggcctgggt ttgcacccaa tttctggaca ttttatagct gagcattaca tgttcttaaa      660
gggtcatgaa acttactcat attatgggcc tctgaattta cttaccttca atgtgggtta      720
tcataatgaa catcatgatt tccccaacat tcctggaaaa agtcttccac tggtgaggaa      780
aatagcagct gaatactatg acaacctccc tctactaat tcctggataa aagtactgta      840
tgattttgtg atggatgata caataagtcc ctactcaaga atgaagaggc accaaaaagg      900
agagatggtg ctggagtaaa tatcattagt gccaaaggga ttcttctcca aaactttaga      960
tgataaaatg gaatttttgc attattaaac ttgagaccag tgatgctcag aagctccctt     1020
ggcacaattt cagagtaaga gctcggtgat accaagaagt gaatctggct tttaaacagt     1080
cagcctgact ctgtactgct cagtttcact cacaggaaac ttgtgacttg tgtattatcg     1140
tcattgagga tgtttcactc atgtctgtca ttttataagc atatcattta aaaagcttct     1200
aaaaagctat ttcgccagg                                     1219
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<210> 28

<211> 655

<212> DNA

<213> Homo sapiens

<400> 28

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gaaccatatt cccatgcaca ttgatcatga ccggaacatg gactggggtt ccaccagct      180
ccaggccaca tgcaatgtcc acaagtctgc cttcaatgac tggttcagtg gacacctcaa      240
cttcagatt gagcaccatc tttttccac gatgcctcga cacaattacc acaaagtggc      300
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tcccctggtg cagtccttgt gtgccaagca tggcatagag taccagtcca agcccctgct	360
gtcagccttc gccgacatca tccactcact aaaggagtca gggcagctct ggctagatgc	420
ctatcttcac caataacaac agccaccctg cccagtctgg aagaagagga ggaagactct	480
ggagccaagg cagaggggag cttgaggggac aatgccacta tagtttaata ctcagagggg	540
gttggggtttg gggacataaa gcctctgact caaactcctc ccttttatct tctagccaca	600
gttctaagac ccaaagtggg ggggtggacac agaagtcctt aggaggggaag gagct	655

<210> 29  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 29	
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tctcaggccc aagctggatg gctgcaacat gattatggcc acctgtctgt ctacagaaaa	120
cccaagtgga accaccttgt ccacaaattc gtcattggcc acttaaaggg tgcctctgcc	180
aactggtgga atcatcgcca cttccagcac cagccaagc ctaacatctt ccacaaggat	240
cccgatgtga acatgctgca cgtgtttgtt ctgggcgaat ggcagcccat cgagtacggc	300
aaga	304

<210> 30  
 <211> 918  
 <212> DNA  
 <213> Homo sapiens

<400> 30	
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ccagggggct cccgggtcat cagccactac gccgggcagg atgccacgga tccctttgtg	180
gccttcaca tcaacaaggg ccttgtgaag aagtatatga actctctcct gattggagaa	240
ctgtctccag agcagcccag ctttgagccc accaagaata aagagctgac agatgagttc	300
cgggagctgc gggccacagt ggagcggatg gggctcatga aggccaacca tgtcttcttc	360
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caggctggct ggctgcagca tgactttggg cacctgtcgg tcttcagcac ctcaaagtgg	540
aaccatctgc tacatcattt tgtgattggc cacctgaagg gggccccgc cagttggtgg	600
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gccttgctgc	ctctctactt	ccagtgggat	atcttctatt	ttgttatcca	gcgaaagaag	840
tgggtggact	tggcctggat	cagcaaacag	gaatacga	aagccgggct	tccattgtcc	900
accgcaaatg	cttctaaa					918

<210> 31  
 <211> 1686  
 <212> DNA  
 <213> Homo sapiens

<400> 31		
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agcctaacat	cttcacaaag	gatcccgatg tgaacatgct gcacgtgttt gttctgggag 120
aatggcagcc	catcgagtac	ggcaagaaga agctgaaata cctgccctac aatcaccagc 180
acgaatactt	cttcttgatt	gggccgccc tgctcatccc catgtatttc cagtaccaga 240
tcatcatgac	catgatcgtc	cataagaact ggggtggacct ggcctgggccc gtcagctact 300
acatccgggt	cttcatcacc	tacatccctt tctacggcat cctgggagcc ctctttttcc 360
tcaacttcat	caggttcctg	gagagccact gggttgtgtg ggtcacacag atgaatcaca 420
tcgtcatgga	gattgaccag	gaggcctacc gtgactgggt cagtagccag ctgacagcca 480
cctgcaacgt	ggagcagtc	ttcttcaacg actgggtcag tggacacctt aacttccaga 540
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acaaatgaag	ccacagcccc	cgggacaccg tggggaaggg gtgcagggtg ggtgatggcc 780
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caacttgagc ctgtgacctt gggaccaaag ggggagtcct tcgtctcttg tgactcagca	1500
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cttttcctca ggggtgtcctg aggtccaaga ttctggagca atctgacct tctccaaagg	1620
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<210> 32  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

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ccaagtgga accaccttgt ccacaaatc gtcattggcc acttaaaggg tgccctctgcc	180
aactggtgga atcatcgcca cttccagcac cagccaagc ctaacatctt ccacaaggat	240
cccgatgtga acatgctgca cgtgtttgtt ctgggcgaat ggcagcccat cgagtacggc	300
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atccctttct acggcatcct gggagccctc cttttcctca acttcacag gttcctggag	540
agccactggg ttgtgtgggt cacacagatg aatcacatcg tcatggagat tgaccaggag	600
gcctaccgtg actggttcag tagccagctg acagccacct gcaacgtgga gcagtccttc	660
ttcaacgact ggttcagtgg acaccttaac ttccagattg agcaccacct ctccccacc	720
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ggcattgaat accaggagaa gccgctactg agggccctgc tggacatcat caggctccctg	840
aagaagtctg ggaagctgtg gctggacgcc taccttcaca aatgaagcca cagcccccg	900
gacaccgtgg ggaaggggtg caggtggggg gatggccaga ggaatgatgg gcttttgttc	960
tgaggggtgt ccgagaggct ggtgtatgca ctgctcaggg accccatgtt ggatctttct	1020
ccctttctcc tctccttttt ctcttcacat ctccccata gcacctgcc ctcatgggac	1080
ctgccctccc tcagccgtca gccatcagcc atggccctcc cagtgcctcc tagcccttc	1140
ttccaaggag cagagagggt gccaccgggg gtggctctgt cctacctcca ctctctgccc	1200

ctaaagatgg gaggagacca gcggtccatg ggtctggcct gtgagtctcc ccttgcagcc	1260
tggctactag gcatcacccc cgcttttggtt cttcagatgc tcttgggggtt cataggggca	1320
ggtcctagtc gggcagggcc cctgaccctc ccggcctggc ttcactctcc ctgacggctg	1380
ccatttgtcc acccttttcat agagaggcct gctttgttac aaagctcggg tctccctcct	1440
gcagctcggg taagtaccgg aggcctctct taagatgtcc agggccccag gcccgcgggc	1500
acagccagcc caaaccttgg gccctggaag agtcctccac cccatcacta gagtgtcttg	1560
accctgggct ttcacgggccc ccattccacc gcctcccaa cttgagcctg tgaccttggg	1620
accaaagggg gagtccctcg tctcttgtga ctcagcagag gcagtggcca cgttcaggga	1680
ggggccggct ggcctggagg ctcagcccac cctccagctt ttcctcaggg tgtcctgagg	1740
tccaagattc tggagcaatc tgacccttct ccaaaggctc tgttatcagc tgggcagtgc	1800
cagccaatcc ctggccattt ggccccaggg gacgtggggc ctg	1843

<210> 33  
 <211> 2257  
 <212> DNA  
 <213> Homo sapiens

<400> 33	
cagggacctt ccccgcgcta cttcacctgg gacgaggtgg cccagcgctc aggggtgcgag	60
gagcgggtgg tagtgatcga ccgtaagggtg tacaacatca gcgagttcac ccgcccggcat	120
ccaggggggt cccgggtcat cagccactac gccgggcagg atgccacgga tccctttgtg	180
gccttccaca tcaacaaggg ccttgtgaag aagtatatga actctctcct gatttgagaa	240
ctgtctccag agcagcccag ctttgagccc accaagaata aagagctgac agatgagttc	300
cgggagctgc gggccacagt ggagcggatg gggctcatga aggccaaacca tgtcttcttc	360
ctgctgtacc tgctgcacat cttgctgctg gatgggtgcag cctgggtcac cctttgggtc	420
tttgggacgt cttttttgcc cttctctctc tgtgcggtgc tgetcagtc agttcagcag	480
gcccagctg gatggctgca acatgattat ggccacctgt ctgtctacag aaaacccaag	540
tggaaccacc ttgtccacaa attcgtcatt ggccacttaa agggtgccctc tgccaactgg	600
tggaatcatc gccacttcca gcaccacgcc aagcctaaca tcttccacaa ggatcccgat	660
gtgaacatgc tgcacgtggt tgttctgggc gaatggcagc ccatcgagta cggcaagaag	720
aagctgaaat acctgcccta caatcaccag cacgaatact tcttctgat tgggccggcg	780
ctgctcatcc ccatgtatct ccagtaccag atcatcatga ccatgatcgt ccataagaac	840
tgggtggacc tggcctgggc cgtcagctac tacatccggg tcttcatcac ctacatccct	900
ttctacggca tcttgggagc cctccttttc ctcaacttca tcaggttctt ggagagccac	960



Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile Met Met  
 20 25 30  
 Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp Leu Asp Trp  
 35 40 45  
 Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser Cys Ile Asn His  
 50 55 60  
 Ser Met Thr Leu Ala Ile His Glu Ile Ala His Asn Ala Ala Phe Gly  
 65 70 75 80  
 Asn Cys Lys Ala Met Trp Asn Arg Trp Phe Gly Met Phe Ala Asn Leu  
 85 90 95  
 Pro Ile Gly Ile Pro Tyr Ser Ile Ser Phe Lys Arg Tyr His Met Asp  
 100 105 110  
 His His Arg Tyr Leu Gly Ala Asp Gly Val Asp Val Asp Ile Pro Thr  
 115 120 125  
 Asp Phe Glu Gly Trp Phe Phe Cys Thr Ala Phe Arg Lys Phe Ile Trp  
 130 135 140  
 Val Ile Leu Gln Pro Leu Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn  
 145 150 155 160  
 Pro Lys Pro Ile Thr Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val  
 165 170 175  
 Thr Phe Asp Ile Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val  
 180 185 190  
 Tyr Met Leu Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser  
 195 200 205  
 Gly His Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr  
 210 215 220  
 Tyr Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr  
 225 230 235 240  
 His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu Pro  
 245 250 255  
 Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro His Tyr  
 260 265 270  
 Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp Asp Thr Ile  
 275 280 285  
 Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly Glu Met Val Leu  
 290 295 300  
 Glu Xaa Ile Ser Leu Val Pro Lys Gly Phe Phe Ser Lys Thr Leu Asp  
 305 310 315 320  
 Asp Lys Met Glu Phe Leu His Tyr Xaa Thr Xaa Asp Gln Xaa Cys Ser  
 325 330 335  
 Glu Ala Pro Leu Ala Gln Phe Gln Ser Lys Ser Ser Val Ile Pro Arg



340	345	350
Ser Glu Ser Gly Phe Xaa Thr Val Ser Leu Thr Leu Tyr Cys Ser Val		
355	360	365
Ser Leu Thr Gly Asn Leu Xaa Leu Val Tyr Tyr Arg His Xaa Gly Cys		
370	375	380
Phe Thr His Val Cys His Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu		
385	390	395
Lys Ser Tyr Phe Ala Arg		
405		

<210> 35  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <221> UNSURE  
 <222> (1)..(218)  
 <223> Amino acids 145,168,174,186,189,198, and 202 uncertain of sequence

<400> 35

Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly Ala		
1	5	10
Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn		
20	25	30
Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met His Ile Asp		
35	40	45
His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys		
50	55	60
Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn		
65	70	75
Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr		
85	90	95
His Lys Val Ala Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile		
100	105	110
Glu Tyr Gln Ser Lys Pro Leu Leu Ser Ala Phe Ala Asp Ile Ile His		
115	120	125
Ser Leu Lys Glu Ser Gly Gln Leu Trp Leu Asp Ala Tyr Leu His Gln		
130	135	140
Xaa Gln Gln Pro Pro Cys Pro Val Trp Lys Lys Arg Arg Lys Thr Leu		
145	150	155
Glu Pro Arg Gln Arg Gly Ala Xaa Gly Thr Met Pro Leu Xaa Phe Asn		
165	170	175

Thr Gln Arg Gly Leu Gly Leu Gly Thr Xaa Ser Leu Xaa Leu Lys Leu  
180 185 190

Leu Pro Phe Ile Phe Xaa Pro Gln Phe Xaa Asp Pro Lys Trp Gly Val  
195 200 205

Asp Thr Glu Val Pro Arg Arg Glu Gly Ala  
210 215

<210> 36

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(87)

<223> Amino acid 87 uncertain of sequence

<400> 36

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe  
1 5 10 15

Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr  
20 25 30

Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His  
35 40 45

Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn  
50 55 60

His Arg His Phe Gln His His Ala Lys Pro Asn Leu Gly Glu Trp Gln  
65 70 75 80

Pro Ile Glu Tyr Gly Lys Xaa  
85

<210> 37

<211> 306

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(306)

<223> Amino acid 252 uncertain of sequence

<400> 37

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln Arg  
1 5 10 15

Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn  
20 25 30

Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg Val Ile Ser

35

40

45

His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile  
 50 55 60  
 Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser Leu Leu Ile Gly Glu  
 65 70 75 80  
 Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro Thr Lys Asn Lys Glu Leu  
 85 90 95  
 Thr Asp Glu Phe Arg Glu Leu Arg Ala Thr Val Glu Arg Met Gly Leu  
 100 105 110  
 Met Lys Ala Asn His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu  
 115 120 125  
 Leu Leu Asp Gly Ala Ala Trp Leu Thr Leu Trp Val Phe Gly Thr Ser  
 130 135 140  
 Phe Leu Pro Phe Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Ala  
 145 150 155 160  
 Gln Ala Gly Trp Leu Gln His Asp Phe Gly His Leu Ser Val Phe Ser  
 165 170 175  
 Thr Ser Lys Trp Asn His Leu Leu His His Phe Val Ile Gly His Leu  
 180 185 190  
 Lys Gly Ala Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His  
 195 200 205  
 Ala Lys Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro  
 210 215 220  
 Phe Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln  
 225 230 235 240  
 Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xaa Tyr Phe Phe Leu  
 245 250 255  
 Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr Ile Phe  
 260 265 270  
 Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala Trp Ile Ser  
 275 280 285  
 Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser Thr Ala Asn Ala  
 290 295 300

Ser Lys  
305

<210> 38  
 <211> 562  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (1)..(562)

<223> Amino acids 242,268,405,438,464,482,497, and 562 uncertain of sequence

<400> 38

His	Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln
1				5					10					15	
His	His	Ala	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met
			20					25					30		
Leu	His	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys
		35					40					45			
Lys	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe
	50					55					60				
Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln	Ile
65					70					75					80
Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala	Trp	Ala
				85					90					95	
Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly
			100					105					110		
Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg	Phe	Leu	Glu	Ser
		115					120					125			
His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	Ile	Val	Met	Glu	Ile
	130					135					140				
Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser	Ser	Gln	Leu	Thr	Ala	Thr
145					150					155					160
Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn	Asp	Trp	Phe	Ser	Gly	His	Leu
				165					170					175	
Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn
		180						185					190		
Leu	His	Lys	Ile	Ala	Pro	Leu	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly
		195					200					205			
Ile	Glu	Tyr	Gln	Glu	Lys	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile
	210					215					220				
Arg	Ser	Leu	Lys	Lys	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His
225					230					235					240
Lys	Xaa	Ser	His	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp
				245					250					255	
Gly	Asp	Gly	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	Xaa	Gly	Val	Ser	Glu
			260					265					270		
Arg	Leu	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro
		275					280					285			
Phe	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His	Leu	Pro	His	Ser	Thr	Leu	Pro

290	295	300
Ser Trp Asp Leu Pro	Ser Leu Ser Arg Gln	Pro Ser Ala Met Ala Leu
305	310	315 320
Pro Val Pro Pro Ser	Pro Phe Phe Gln Gly	Ala Glu Arg Trp Pro Pro
	325	330 335
Gly Val Ala Leu Ser	Tyr Leu His Ser	Leu Pro Leu Lys Met Gly Gly
	340	345 350
Asp Gln Arg Ser Met	Gly Leu Ala Cys Glu	Ser Pro Leu Ala Ala Trp
	355	360 365
Ser Leu Gly Ile Thr	Pro Ala Leu Val Leu	Gln Met Leu Leu Gly Phe
	370	375 380
Ile Gly Ala Gly Pro	Ser Arg Ala Gly Pro	Leu Thr Leu Pro Ala Trp
385	390	395 400
Leu His Ser Pro Xaa	Arg Leu Pro Leu Val	His Pro Phe Ile Glu Arg
	405	410 415
Pro Ala Leu Leu Gln	Ser Ser Gly Leu Pro	Pro Ala Ala Arg Leu Ser
	420	425 430
Thr Arg Gly Leu Ser	Xaa Asp Val Gln Gly	Pro Arg Pro Ala Gly Thr
	435	440 445
Ala Ser Pro Asn Leu	Gly Pro Trp Lys Ser	Pro Pro His His Xaa
450	455	460
Ser Ala Leu Thr Leu	Gly Phe His Gly Pro	His Ser Thr Ala Ser Pro
465	470	475 480
Thr Xaa Ala Cys Asp	Leu Gly Thr Lys Gly	Gly Val Pro Arg Leu Leu
	485	490 495
Xaa Leu Ser Arg Gly	Ser Gly His Val Gln	Gly Gly Ala Gly Trp Pro
	500	505 510
Gly Gly Ser Ala His	Pro Pro Ala Phe Pro	Gln Gly Val Leu Arg Ser
	515	520 525
Lys Ile Leu Glu Gln	Ser Asp Pro Ser Pro	Lys Ala Leu Leu Ser Ala
	530	535 540
Gly Gln Cys Gln Pro	Ile Pro Gly His Leu	Ala Pro Gly Asp Val Gly
545	550	555 560

Pro Xaa

<210> 39  
 <211> 615  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> UNSURE  
 <222> (1)..(615)

<223> Amino acids 295,321,458,491,517,535,550, and 615 uncertain of sequence

<400> 39

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe  
1 5 10 15

Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr  
20 25 30

Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His  
35 40 45

Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn  
50 55 60

His Arg His Phe Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp  
65 70 75 80

Pro Asp Val Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro  
85 90 95

Ile Glu Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln  
100 105 110

His Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr  
115 120 125

Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val  
130 135 140

Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr  
145 150 155 160

Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile  
165 170 175

Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His  
180 185 190

Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser  
195 200 205

Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp  
210 215 220

Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr  
225 230 235 240

Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu  
245 250 255

Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala  
260 265 270

Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu  
275 280 285

Asp Ala Tyr Leu His Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly

290	295	300
Lys Gly Cys Arg Trp 305	Gly Asp Gly Gln Arg 310	Asn Asp Gly Leu Leu Phe 315 320
Xaa Gly Val Ser 325	Glu Arg Leu Val Tyr 330	Ala Leu Leu Thr Asp Pro Met 335
Leu Asp Leu Ser 340	Pro Phe Leu Leu Ser 345	Phe Phe Ser Ser His Leu Pro 350
His Ser Thr 355	Leu Pro Ser Trp Asp 360	Leu Ser Arg Gln Pro 365
Ser Ala Met Ala Leu Pro 370	Val Pro Pro Ser Pro 375	Phe Phe Gln Gly Ala 380
Glu Arg Trp Pro Pro 385	Gly Val Ala Leu Ser 390	Tyr Leu His Ser Leu Pro 395 400
Leu Lys Met Gly 405	Gly Asp Gln Arg Ser 410	Met Gly Leu Ala Cys Glu Ser 415
Pro Leu Ala Ala Trp 420	Ser Leu Gly Ile Thr 425	Pro Ala Leu Val Leu Gln 430
Met Leu Leu Gly Phe Ile 435	Gly Ala Gly Pro Ser 440	Arg Ala Gly Pro Leu 445
Thr Leu Pro Ala Trp 450	Leu His Ser Pro Xaa 455	Arg Leu Pro Leu Val His 460
Pro Phe Ile Glu Arg 465	Pro Ala Leu Leu Gln 470	Ser Ser Gly Leu Pro Pro 475 480
Ala Ala Arg Leu Ser 485	Thr Arg Gly Leu Ser 490	Xaa Asp Val Gln Gly Pro 495
Arg Pro Ala Gly Thr 500	Ala Ser Pro Asn Leu 505	Gly Pro Trp Lys Ser Pro 510
Pro Pro His His Xaa Ser 515	Ala Leu Thr Leu Gly 520	Phe His Gly Pro His 525
Ser Thr Ala Ser Pro 530	Thr Xaa Ala Cys Asp 535	Leu Gly Thr Lys Gly Gly 540
Val Pro Arg Leu Leu 545	Xaa Leu Ser Arg Gly 550	Ser Gly His Val Gln Gly 555 560
Gly Ala Gly Trp Pro 565	Gly Gly Ser Ala His 570	Pro Pro Ala Phe Pro Gln 575
Gly Val Leu Arg Ser 580	Lys Ile Leu Glu Gln 585	Ser Asp Pro Ser Pro Lys 590
Ala Leu Leu Ser Ala Gly 595	Gln Cys Gln Pro Ile 600	Pro Gly His Leu Ala 605
Pro Gly Asp Val Gly 610	Pro Xaa 615	

<210> 40  
<211> 753  
<212> PRT  
<213> Homo sapiens

<220>  
<221> UNSURE  
<222> (1)..(753)  
<223> Amino acids 433,459,596,629,655,673,688, and 753 uncertain of sequence

<400> 40

Gln	Gly	Pro	Thr	Pro	Arg	Tyr	Phe	Thr	Trp	Asp	Glu	Val	Ala	Gln	Arg	
1				5					10					15		
Ser	Gly	Cys	Glu	Glu	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val	Tyr	Asn	
			20					25					30			
Ile	Ser	Glu	Phe	Thr	Arg	Arg	His	Pro	Gly	Gly	Ser	Arg	Val	Ile	Ser	
		35					40					45				
His	Tyr	Ala	Gly	Gln	Asp	Ala	Thr	Asp	Pro	Phe	Val	Ala	Phe	His	Ile	
	50					55					60					
Asn	Lys	Gly	Leu	Val	Lys	Lys	Tyr	Met	Asn	Ser	Leu	Leu	Ile	Gly	Glu	
65					70					75					80	
Leu	Ser	Pro	Glu	Gln	Pro	Ser	Phe	Glu	Pro	Thr	Lys	Asn	Lys	Glu	Leu	
				85					90					95		
Thr	Asp	Glu	Phe	Arg	Glu	Leu	Arg	Ala	Thr	Val	Glu	Arg	Met	Gly	Leu	
			100					105					110			
Met	Lys	Ala	Asn	His	Val	Phe	Phe	Leu	Leu	Tyr	Leu	Leu	His	Ile	Leu	
		115					120					125				
Leu	Leu	Asp	Gly	Ala	Ala	Trp	Leu	Thr	Leu	Trp	Val	Phe	Gly	Thr	Ser	
	130					135					140					
Phe	Leu	Pro	Phe	Leu	Leu	Cys	Ala	Val	Leu	Leu	Ser	Ala	Val	Gln	Gln	
145					150					155					160	
Ala	Gln	Ala	Gly	Trp	Leu	Gln	His	Asp	Tyr	Gly	His	Leu	Ser	Val	Tyr	
				165					170					175		
Arg	Lys	Pro	Lys	Trp	Asn	His	Leu	Val	His	Lys	Phe	Val	Ile	Gly	His	
			180					185					190			
Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln	His	
		195					200					205				
His	Ala	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	
	210					215					220					
His	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	
225					230					235					240	
Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	Leu	
				245					250					255		



Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile  
 260 265 270  
 Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val  
 275 280 285  
 Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile  
 290 295 300  
 Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His  
 305 310 315 320  
 Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp  
 325 330 335  
 Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys  
 340 345 350  
 Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn  
 355 360 365  
 Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu  
 370 375 380  
 His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile  
 385 390 395 400  
 Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg  
 405 410 415  
 Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys  
 420 425 430  
 Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly  
 435 440 445  
 Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg  
 450 455 460  
 Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe  
 465 470 475 480  
 Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser  
 485 490 495  
 Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro  
 500 505 510  
 Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly  
 515 520 525  
 Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly Asp  
 530 535 540  
 Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala Trp Ser  
 545 550 555 560  
 Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu Gly Phe Ile  
 565 570 575

Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu  
580 585 590

His Ser Pro Xaa Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro  
595 600 605

Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr  
610 615 620

Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala  
625 630 635 640

Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser  
645 650 655

Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro Thr  
660 665 670

Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa  
675 680 685

Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly  
690 695 700

Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys  
705 710 715 720

Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly  
725 730 735

Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro  
740 745 750

Xaa

C1  
cont